RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/582,779

Source: 1636

Date Processed by STIC: 1/19/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW.**

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/582,779_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                               This may occur if your file was retrieved in a word processor after creating it.
                               Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                               This may occur if your file was retrieved in a word processor after creating it.
                               Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                               Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                               As per the rules, each n or Xaa can only represent a single residue.
                               Please present the maximum number of each residue having variable length and
                               indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                               sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                               to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
                               sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X:
                               (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                               This sequence is intentionally skipped

                               Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   <210> sequence id number
                               <400> sequence id number
                               000

10 ✓ Use of n's or Xaa's,   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

                               3-6.

12 ✓ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                               Please explain source of genetic material in <220> to <223> section.
                               (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
                               file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                               Instead, please use "File Manager" or any other means to copy file to floppy disk.

```
                RAW SEQUENCE LISTING              DATE: 01/19/2001
                PATENT APPLICATION:  US/09/582,779   TIME: 14:17:11
```

Does Not Comply
Corrected Diskette Needed

```
                Input Set : A:\ES.txt
                Output Set: N:\CRF3\01192001\I582779.raw

         3 <110> APPLICANT: Pompejus, Markus
         4         Doval, Jose Luis Revuelta
         5         Garcia, Maria Angeles Santos
         7 <120> TITLE OF INVENTION: Orotidine-5'-phosphate decarboxylase gene, gene construct comprising
         8         this gene and its use.
         0 <130> FILE REFERENCE:
        10 <140> CURRENT APPLICATION NUMBER: US 09/582,779
        11 <141> CURRENT FILING DATE: 2000-07-03
        13 <150> PRIOR APPLICATION NUMBER: Germany/19801120.2
        14 <151> PRIOR FILING DATE: 1998-01-15
E--> 16 <160> NUMBER OF SEQ ID NOS: 5    6 (next page)
        18 <170> SOFTWARE: WordPerfect Version 6.1


    ERRORED SEQUENCES

       180 <210> SEQ ID NO: 3
       181 <211> LENGTH: 18
       182 <212> TYPE: DNA
       183 <213> ORGANISM: Artificial sequence
       185 <220> FEATURE:
       186 <221> NAME/KEY: misc_feature
       187 <222> LOCATION: 1 ... 18
W--> 189 <223> OTHER INFORMATION:
       189 <400> SEQUENCE: 3
E--> 191 ytnggncqnt ayathtgy
       194 <210> SEQ ID NO: 4
       195 <211> LENGTH: 23
       196 <212> TYPE: DNA
       197 <213> ORGANISM: Artificial sequence
       199 <220> FEATURE:
       200 <221> NAME/KEY: misc_feature
       201 <222> LOCATION: 1 ... 23
W--> 203 <223> OTHER INFORMATION:
       203 <400> SEQUENCE: 4
E--> 205 taytgytgnt qnaryttrtc ntc
       208 <210> SEQ ID NO: 5
       209 <211> LENGTH: 26
       210 <212> TYPE: DNA
       211 <213> ORGANISM: Artificial sequence
       213 <220> FEATURE:
       214 <221> NAME/KEY: misc_feature
       215 <222> LOCATION: 1 ... 26
W--> 217 <223> OTHER INFORMATION:
       217 <400> SEQUENCE: 5
E--> 219 ttyytnatht tygargaymg nnaartt
       222 <210> SEQ ID NO: 6
```

(handwritten annotations):
OK

Global errors

see item 12 on Erra Summary Sheet

→ see item 10 on Erra Summary Sheet

18↑ insert cumulative base total at right margin of each line

same error

↓23

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779

DATE: 01/19/2001
TIME: 14:17:11

Input Set : A:\ES.txt
Output Set: N:\CRF3\01192001\I582779.raw

```
        223 <211> LENGTH: 19
        224 <212> TYPE: DNA
        225 <213> ORGANISM: Artificial sequence
        227 <220> FEATURE:
        228 <221> NAME/KEY: misc_feature
        229 <222> LOCATION: 1 ... 19
W-->    231 <223> OTHER INFORMATION:
        231 <400> SEQUENCE: 6
E-->    233 gcnarnarna rnarncnc
```

last sequence in file

total
6

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/582,779

DATE: 01/19/2001
TIME: 14:17:12

Input Set : A:\ES.txt
Output Set: N:\CRF3\01192001\I582779.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:189 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:191 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3
L:203 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:205 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:4
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:233 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (6)